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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/454,223DATE: 12/27/1999
TIME: 12:42:18

Input Set: I454223.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

ENTERED

1 <110> APPLICANT: Kornbluth, Richard S
2 <120> TITLE OF INVENTION: Multimeric forms of CD40L and other TNF family members
3 <130> FILE REFERENCE: TNFSF-collectin fusion proteins
4 <140> CURRENT APPLICATION NUMBER: US/09/454,223
5 <141> CURRENT FILING DATE: 1999-12-09
6 <160> NUMBER OF SEQ ID NOS: 6
7 <170> SOFTWARE: PatentIn Ver. 2.1
8 <210> SEQ ID NO 1
9 <211> LENGTH: 1552
10 <212> TYPE: DNA
11 <213> ORGANISM: Artificial Sequence
12 <220> FEATURE:
13 <221> NAME/KEY: 5'UTR
14 <222> LOCATION: (7)..(31)
15 <220> FEATURE:
16 <221> NAME/KEY: misc_feature
17 <222> LOCATION: (88)..(799)
18 <223> OTHER INFORMATION: Mature murine surfactant protein D including hub
19 region, collagenous portion, and neck, but
20 excluding carbohydrate recognition domain (CRD)
21 <220> FEATURE:
22 <221> NAME/KEY: misc_feature
23 <222> LOCATION: (801)..(1546)
24 <223> OTHER INFORMATION: Human CD40 ligand extracellular region, including
25 stalk.
26 <220> FEATURE:
27 <221> NAME/KEY: sig_peptide
28 <222> LOCATION: (32)..(88)
29 <223> OTHER INFORMATION: Signal peptide from murine surfactant protein D
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (32)..(1444)
33 <220> FEATURE:
34 <223> OTHER INFORMATION: Description of Artificial Sequence: Murine
35 surfactant protein D (without the CRD) fused to
36 the extracellular portion of human CD40L
37 <300> PUBLICATION INFORMATION:
38 <301> AUTHORS: Spriggs, Melanie K.
39 Armitage, Richard J.
40 Strockbine, L
41 Clifford, K N.
42 Macduff, B M.
43 Sato, T.A.
44 Maliszewski, C R.

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45      Fanslow, William C.
46 <302> TITLE: Recombinant human CD40 ligand stimulates B cell
47      proliferation and immunoglobulin E secretion.
48 <303> JOURNAL: J. Exp. Med.
49 <304> VOLUME: 176
50 <305> ISSUE: 6
51 <306> PAGES: 1543-1550
52 <307> DATE: 1992
53 <313> RELEVANT RESIDUES: 801 TO 1600
54 <300> PUBLICATION INFORMATION:
55 <301> AUTHORS: Motwani, M
56 <302> TITLE: Mouse surfactant protein-D.      cDNA cloning,
57 <303> JOURNAL: J. Immunol.
58 <304> VOLUME: 155
59 <305> ISSUE: 12
60 <306> PAGES: 5671-5677
61 <307> DATE: 1995
62 <313> RELEVANT RESIDUES: 32 TO 800
63 <400> SEQUENCE: 1
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67      ctt gtc ttg ctt gta cag ccc ctg gga aat ctg gga gca gaa atg aag      100
68      Leu Val Leu Leu Val Gln Pro Leu Gly Asn Leu Gly Ala Glu Met Lys
69               10               15               20
70      agc ctc tcg cag aga tca gta ccc aac acc tgc acc cta gtc atg tgt      148
71      Ser Leu Ser Gln Arg Ser Val Pro Asn Thr Cys Thr Leu Val Met Cys
72               25               30               35
73      agc cca aca gag aat ggc ctg cct ggt cgt gat gga cgg gat ggg aga      196
74      Ser Pro Thr Glu Asn Gly Leu Pro Gly Arg Asp Gly Arg Asp Gly Arg
75      40               45               50               55
76      gaa ggt cca cgg ggt gag aag ggt gat cca ggt ttg cca gga cct atg      244
77      Glu Gly Pro Arg Gly Glu Lys Gly Asp Pro Gly Leu Pro Gly Pro Met
78               60               65               70
79      ggg ctc tca ggg ttg cag ggc cct aca ggt cca gtt gga ccc aaa gga      292
80      Gly Leu Ser Gly Leu Gln Gly Pro Thr Gly Pro Val Gly Pro Lys Gly
81               75               80               85
82      gag aat ggc tct gct ggc gaa cct gga cca aag gga gaa cgt gga cta      340
83      Glu Asn Gly Ser Ala Gly Glu Pro Gly Pro Lys Gly Glu Arg Gly Leu
84               90               95               100
85      agt gga cct cca gga ctt cca ggt att cct ggt cca gct ggg aaa gaa      388
86      Ser Gly Pro Pro Gly Leu Pro Gly Ile Pro Gly Pro Ala Gly Lys Glu
87               105               110               115
88      ggt ccc tct ggg aag cag ggg aac ata gga cct caa ggc aaa cca ggt      436
89      Gly Pro Ser Gly Lys Gln Gly Asn Ile Gly Pro Gln Gly Lys Pro Gly
90      120               125               130               135
91      cct aaa gga gag gct ggg ccc aaa gga gaa gta ggt gct cct ggc atg      484
92      Pro Lys Gly Glu Ala Gly Pro Lys Gly Glu Val Gly Ala Pro Gly Met
93               140               145               150
94      caa gga tct aca ggg gca aaa ggc tcc aca ggc ccc aag gga gaa aga      532

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98	Gly Ala Pro Gly Val Gln Gly Ala Pro Gly Asn Ala Gly Ala Ala Gly	
99	170 175 180	
100	cct gcc gga cct gcc ggt cca cag gga gct cca ggt tcc agg ggg ccc	628
101	Pro Ala Gly Pro Ala Gly Pro Gln Gly Ala Pro Gly Ser Arg Gly Pro	
102	185 190 195	
103	cca gga ctc aag ggg gac aga ggt gtt cct gga gac aga gga atc aaa	676
104	Pro Gly Leu Lys Gly Asp Arg Gly Val Pro Gly Asp Arg Gly Ile Lys	
105	200 205 210 215	
106	ggt gaa agc ggg ctt cca gac agt gct gct ctg agg cag cag atg gag	724
107	Gly Glu Ser Gly Leu Pro Asp Ser Ala Ala Leu Arg Gln Gln Met Glu	
108	220 225 230	
109	gcc tta aaa gga aaa cta cag cgt cta gag gtt gcc ttc tcc cac tat	772
110	Ala Leu Lys Gly Lys Leu Gln Arg Leu Glu Val Ala Phe Ser His Tyr	
111	235 240 245	
112	cag aaa gct gca ttg ttc cct gat ggc cat aga agg ttg gac aag ata	820
113	Gln Lys Ala Ala Leu Phe Pro Asp Gly His Arg Arg Leu Asp Lys Ile	
114	250 255 260	
115	gaa gat gaa agg aat ctt cat gaa gat ttt gta ttc atg aaa acg ata	868
116	Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val Phe Met Lys Thr Ile	
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118	cag aga tgc aac aca gga gaa aga tcc tta tcc tta ctg aac tgt gag	916
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121	gag att aaa agc cag ttt gaa ggc ttt gtg aag gat ata atg tta aac	964
122	Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys Asp Ile Met Leu Asn	
123	300 305 310	
124	aaa gag gag acg aag aaa gaa aac agc ttt gaa atg caa aaa ggt gat	1012
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127	cag aat cct caa att gcg gca cat gtc ata agt gag gcc agc agt aaa	1060
128	Gln Asn Pro Gln Ile Ala Ala His Val Ile Ser Glu Ala Ser Ser Lys	
129	330 335 340	
130	aca aca tct gtg tta cag tgg gct gaa aaa gga tac tac acc atg agc	1108
131	Thr Thr Ser Val Leu Gln Trp Ala Glu Lys Gly Tyr Tyr Thr Met Ser	
132	345 350 355	
133	aac aac ttg gta acc ctg gaa aat ggg aaa cag ctg acc gtt aaa aga	1156
134	Asn Asn Leu Val Thr Leu Glu Asn Gly Lys Gln Leu Thr Val Lys Arg	
135	360 365 370 375	
136	caa gga ctc tat tat atc tat gcc caa gtc acc ttc tgt tcc aat cgg	1204
137	Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln Val Thr Phe Cys Ser Asn Arg	
138	380 385 390	
139	gaa gct tcg agt caa gct cca ttt ata gcc agc ctc tgc cta aag tcc	1252
140	Glu Ala Ser Ser Gln Ala Pro Phe Ile Ala Ser Leu Cys Leu Lys Ser	
141	395 400 405	
142	ccc ggt aga ttc gag aga atc tta ctc aga gct gca aat acc cac agt	1300
143	Pro Gly Arg Phe Glu Arg Ile Leu Leu Arg Ala Ala Asn Thr His Ser	
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149      Glu Leu Gln Pro Gly Ala Ser Val Phe Val Asn Val Thr Asp Pro Ser
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151      caa gtg agc cat ggc act ggc ttc acg tcc ttt ggc tta ctc aaa ctc      1444
152      Gln Val Ser His Gly Thr Gly Phe Thr Ser Phe Gly Leu Leu Lys Leu
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154      tgaacagtgt caccttgacg gctgtggtgg agctgacgct gggagtcttc ataatacagc      1504
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158 <212> TYPE: PRT
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161 <223> OTHER INFORMATION: Description of Artificial Sequence: Murine
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163      the extracellular portion of human CD40L
164 <400> SEQUENCE: 2
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168          20                      25                      30
169      Thr Cys Thr Leu Val Met Cys Ser Pro Thr Glu Asn Gly Leu Pro Gly
170          35                      40                      45
171      Arg Asp Gly Arg Asp Gly Arg Glu Gly Pro Arg Gly Glu Lys Gly Asp
172          50                      55                      60
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174          65                      70                      75                      80
175      Gly Pro Val Gly Pro Lys Gly Glu Asn Gly Ser Ala Gly Glu Pro Gly
176          85                      90                      95
177      Pro Lys Gly Glu Arg Gly Leu Ser Gly Pro Pro Gly Leu Pro Gly Ile
178          100                     105                     110
179      Pro Gly Pro Ala Gly Lys Glu Gly Pro Ser Gly Lys Gln Gly Asn Ile
180          115                     120                     125
181      Gly Pro Gln Gly Lys Pro Gly Pro Lys Gly Glu Ala Gly Pro Lys Gly
182          130                     135                     140
183      Glu Val Gly Ala Pro Gly Met Gln Gly Ser Thr Gly Ala Lys Gly Ser
184          145                     150                     155                     160
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188          180                     185                     190
189      Ala Pro Gly Ser Arg Gly Pro Pro Gly Leu Lys Gly Asp Arg Gly Val
190          195                     200                     205
191      Pro Gly Asp Arg Gly Ile Lys Gly Glu Ser Gly Leu Pro Asp Ser Ala
192          210                     215                     220
193      Ala Leu Arg Gln Gln Met Glu Ala Leu Lys Gly Lys Leu Gln Arg Leu
194          225                     230                     235                     240

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195      Glu Val Ala Phe Ser His Tyr Gln Lys Ala Ala Leu Phe Pro Asp Gly
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198                      260                      265                      270
199      Phe Val Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser
200                      275                      280                      285
201      Leu Ser Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe
202                      290                      295                      300
203      Val Lys Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Glu Asn Ser
204      305                      310                      315                      320
205      Phe Glu Met Gln Lys Gly Asp Gln Asn Pro Gln Ile Ala Ala His Val
206                      325                      330                      335
207      Ile Ser Glu Ala Ser Ser Lys Thr Thr Ser Val Leu Gln Trp Ala Glu
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209      Lys Gly Tyr Tyr Thr Met Ser Asn Asn Leu Val Thr Leu Glu Asn Gly
210                      355                      360                      365
211      Lys Gln Leu Thr Val Lys Arg Gln Gly Leu Tyr Tyr Ile Tyr Ala Gln
212                      370                      375                      380
213      Val Thr Phe Cys Ser Asn Arg Glu Ala Ser Ser Gln Ala Pro Phe Ile
214      385                      390                      395                      400
215      Ala Ser Leu Cys Leu Lys Ser Pro Gly Arg Phe Glu Arg Ile Leu Leu
216                      405                      410                      415
217      Arg Ala Ala Asn Thr His Ser Ser Ala Lys Pro Cys Gly Gln Gln Ser
218                      420                      425                      430
219      Ile His Leu Gly Gly Val Phe Glu Leu Gln Pro Gly Ala Ser Val Phe
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225 <210> SEQ ID NO 3
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230 <221> NAME/KEY: 5'UTR
231 <222> LOCATION: (7)..(31)
232 <223> OTHER INFORMATION: 5' UTR taken from rat sequence for surfactant
233      protein D
234 <220> FEATURE:
235 <221> NAME/KEY: sig_peptide
236 <222> LOCATION: (32)..(88)
237 <223> OTHER INFORMATION: Signal peptide from murine surfactant protein D
238 <220> FEATURE:
239 <221> NAME/KEY: CDS
240 <222> LOCATION: (32)..(1534)
241 <220> FEATURE:
242 <221> NAME/KEY: misc_feature
243 <222> LOCATION: (32)..(800)
244 <223> OTHER INFORMATION: Murine surfactant protein D including hub region,

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VERIFICATION SUMMARY
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Line ? Error/Warning

Original Text
